

OM protein - protein search, using sw model
Run on: March 14, 2001, 16:12:15 ; Search time 14.09 Seconds
(without alignments)
578.602 Million cell updates/sec

Title: US-09-455-486-6
perfect score: 2351
Sequence: 1 MESISNGSPKSLSETCLPN.....ALVLESVIVIDLQLCRYPTD 454

scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 179772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

DB seq length: 0

Max DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/pctodata/2/iaa/5A/COMB.pep:
2: /cgn2_6/pctodata/2/iaa/5B/COMB.pep:
3: /cgn2_6/pctodata/2/iaa/6_COMB.pep:
4: /cgn2_6/pctodata/2/iaa/PCTRUS/COMB.pep:
5: /cgn2_6/pctodata/2/iaa/backfile1.pep:
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*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	736		31.3	141	3	US-09-083-521-1	Sequence 1, Appli
2	107.5		4.6	695	1	US-08-482-886-2	Sequence 2, Appli
3	107.5		4.6	695	3	US-08-482-855-2	Sequence 2, Appli
4	99		4.2	531	2	US-08-724-974A-2	Sequence 2, Appli
5	97.5		4.1	390	3	US-08-450-576-2	Sequence 2, Appli
6	93		4.0	365	2	US-08-724-974A-3	Sequence 3, Appli
7	89.5		3.8	495	1	US-08-841-99A-2	Sequence 2, Appli
8	89.5		3.8	495	1	US-08-290-301-2	Sequence 2, Appli
9	89.5		3.8	495	2	US-08-588-983-2	Sequence 2, Appli
10	89.5		3.8	495	2	US-08-976-2	Sequence 2, Appli
11	89.5		3.8	968	3	US-08-651-99A-7	Sequence 7, Appli
12	89		3.8	1582	2	US-08-404-531B-9	Sequence 9, Appli
13	89		3.8	1582	3	US-08-476-900A-9	Sequence 9, Appli
14	89		3.8	1582	3	US-08-486-546A-9	Sequence 9, Appli
15	88.5		3.8	591	1	US-08-484-840-2	Sequence 2, Appli
16	88.5		3.8	591	2	US-08-483-094-2	Sequence 2, Appli
17	87		3.7	467	2	US-08-805-118-3	Sequence 3, Appli
18	86.5		3.7	699	1	US-08-348-006B-7	Sequence 7, Appli
19	86.5		3.7	699	2	US-08-800-825A-7	Sequence 2, Appli
20	85.5		3.6	861	3	US-09-022-875-2	Sequence 2, Appli
21	85		3.6	1581	2	US-08-404-531B-6	Sequence 6, Appli
22	85		3.6	1581	3	US-08-476-900A-6	Sequence 6, Appli
23	85		3.6	1581	3	US-08-488-546A-6	Sequence 6, Appli
24	84.5		3.6	550	1	US-08-121-057-4	Sequence 4, Appli
25	84.5		3.6	550	2	US-08-509-187D-4	Sequence 4, Appli
26	84.5		3.6	550	4	PCT-US93-0970A-4	Sequence 4, Appli
27	84.5		3.6	323	2	US-08-580-545B-2	Sequence 2, Appli

STRANDEDNESS: single

TYPE: amino acid

SEQUENCE CHARACTERISTICS:

IMMEDIATE SOURCE:

LIBRARY: PROSUT10

CLOSE: 1691243

US-09-083-521-1

Query Match Similarity 100.0%; Pred. No. 5.9e-70;
Matches 141; Conservative 0; Mismatches 0; Gaps 0;

Score 736; DB 3; Length 141;
Best Local Similarity 100.0%; Pred. No. 5.9e-70;
Matches 141; Conservative 0; Mismatches 0; Gaps 0;
Qy 314 MWVAVSLCLPRLRHSERYLFLNAYAOVHANENSWEEVRRIWYKISFGMSLGLSL 373

ALIGNMENTS

29	84	3.6	323	3	US-09-262-653A-2	Sequence 2, Appli
30	84	3.6	480	2	US-08-724-394A-9	Sequence 9, Appli
31	82.5	3.5	339	3	US-08-968-563-14	Sequence 14, Appli
32	82.5	3.5	339	3	US-08-683A-14	Sequence 14, Appli
33	81	3.4	523	2	US-08-473-553A-3	Sequence 3, Appli
34	81	3.4	980	2	US-08-473-553A-6	Sequence 6, Appli
35	81	3.4	985	2	US-08-473-553A-2	Sequence 2, Appli
36	80.5	3.4	214	1	US-08-318-492-4	Sequence 4, Appli
37	80.5	3.4	214	1	US-08-740-440-4	Sequence 4, Appli
38	80.5	3.4	214	2	US-08-316-302A-3	Sequence 3, Appli
39	80.5	3.4	214	2	US-08-994-578-4	Sequence 4, Appli
40	80.5	3.4	214	2	US-09-13-389-3	Sequence 3, Appli
41	80	3.4	360	3	US-08-875-573-20	Sequence 2, Appli
42	79.5	3.4	354	1	US-07-759-558-2	Sequence 8, Appli
43	79.5	3.4	920	3	US-08-930-596A-8	Sequence 10, Appli
44	79.5	3.4	2366	1	US-08-480-804A-10	Sequence 10, Appli
45	79.5	3.4	2366	2	US-08-405-496A-10	Sequence 10, Appli

102(c) = 05/z2/98

RESULT 1
US-09-083-521-1
; Sequence 1, Application US/09083521
; Patent No. 6048970
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Gusgler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3114 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,521
FILING DATE: Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERONE, MICHAEL C.
REGISTRATION NUMBER: 39-1132
REFERRAL/DOCKET NUMBER: PE-0527 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSUT10
CLOSE: 1691243
US-09-083-521-1

RESULT 2
 US-08-487-886-2
 Sequence 2, Application US/08487886
 Patent No. 5744448

GENERAL INFORMATION:
 APPLICANT: Kelton, Christie Ann
 APPLICANT: Schweickhardt, Rene Lynn
 APPLICANT: Chang, Shirley Yui Yen
 APPLICANT: Nugent, No. 5744446en Patrice
 TITLE OF INVENTION: Hormone Receptor Stimulating
 NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Stephan P. Williams,
 ADDRESS: Area-Serono, Inc.
 STREET: Exchange Place, 37th floor
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
 COMPUTER: IBM PS/2, model 55 SX
 OPERATING SYSTEM: MS-DOS version 4.0
 SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,886
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/670,085
 FILING DATE: 15-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams, Stephan P.
 REGISTRATION NUMBER: 28546

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 723-1300
 TELEFAX: (617) 723-8923

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 695
 TYPE: Amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: Protein

FEATURE:
 NAME/KEY: signal sequence
 LOCATION: 1 to 349
 IDENTIFICATION METHOD: similarity with other
 IDENTIFICATION METHOD: dimeric glycoprotein receptor extracellular
 IDENTIFICATION METHOD: domains, hydrophilic

FEATURE:
 NAME/KEY: transmembrane domain
 LOCATION: 350 to 613
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length

NAME/KEY: putative transmembrane region III
 LOCATION: 382 to 404
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length

NAME/KEY: putative transmembrane region IV
 LOCATION: 469 to 491
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length

NAME/KEY: putative transmembrane region V
 LOCATION: 512 to 533
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length

NAME/KEY: putative transmembrane region VI
 LOCATION: 557 to 580
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length

NAME/KEY: putative transmembrane region VII
 LOCATION: 592 to 613
 IDENTIFICATION METHOD: similarity to other G
 IDENTIFICATION METHOD: protein coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length

NAME/KEY: putative carboxy-terminal intracellular
 LOCATION: 614 to 678

US-08-487-886-2

Query Match 4.6% Score 107.5; DB 1: Length 695;
 Best Local Similarity 17.0%; Pred. No. 0.01%;
 Matches 84; Conservative 77; Mismatches 148; Indels 185; Gaps 17;

QY 79 HEDALTKTNNLIVFHREHTYTSLWDLRHLYG-----KILIDVSNNMR 121
 Db 98 HEIRIEKANL-LYINPEAFQNLNPLOYLJISNTGKHLPDVKTHSLQKVLDIQRN 156

QY 122 INQYEPSEAYLASLIPDSLLVKGENVVAWALQGPDKDASROVYCNSNTOAQVTEL 181
 Db 157 IH-----TIERNSFVLGSFESVTLWL---NKNGIOEHNCA----- 189

QY 182 AROLNFPIDGLSISARETENPLPRLFLIWWRGPVVVAASLATFFFLYSFVDRVTHPYAR 241
 Db 190 --PFGTQDELNSDNNNDELPNDVFGASGPVILDSRTRHSPLPYGLENUKKLR 246

OY 242 NOOSDFYKPIEIVNKTL-PIVATLLSLVY-----
 Db 247 RSTVNKLKP-----TLPKVALMEASUTPSHCCAFANWRQISELPMCKNSILRQ 300

OY 272 -----LAGLLAAAYQLYYGTYYRFF-----PPPLETMQCRKQL 305
 Db 301 VDYMQTQTRGSSLAEDNQSSYSSRCFDMMTYTEFDVDCMEVVDTCSPPDAFPNCEDM 360

OY 306 G-----LSAFFFAMYHVA-----YSCLCPMRSERYFLNMAQYQWHANTE 347